SEQUENCE LISTING

<110> Aehle, Wolfgang
Ramer, Sandra W
Schellenberger, Volker

<120> Generation of Stabilized Proteins by Combinatorial Consensus
Mutagenesis

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<140> US 10/688,255
<141> 2003-10-16

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<170> PatentIn version 3.2

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Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
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Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
    50                  55                  60
Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
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Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala
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Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile
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Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly
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Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr
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Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
    50   55   60
Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65   70   75   80

<210> 8
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223>   consensus mutation

<400> 8

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
1   5   10   15
Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
                20   25   30
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
        35   40   45
Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
    50   55   60
Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
65   70   75   80

<210> 9
<211> 84
<212> PRT
<213> Artificial Sequence

<220>
<223>   consensus mutation

<400> 9

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
1   5   10   15
Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
                20   25   30
Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
        35   40   45
Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln

7

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      50                    55                    60
Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
65                    70                    75                    80
Lys Arg Ala Ala


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<400>  42
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acccactcac gttcggtggc ggcaccaagc tggagct   37

FIGURE 10.

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Translation of CAB1   (1)  QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTDTSSNTAY  (SEQ ID NO:7)
      human consensus (1)  Q            KP G      TFS     V A G                         RF I R   K

                       81                                                         160
Translation of CAB1   (81) LQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSSGGGGSGGGGSGGGGSENVLTQSPAIMSASPGEKVTITCSA  (SEQ ID NO:8)
      human consensus (81)                     AR                                QS    P S V    QT

                       161                                                        240
Translation of CAB1  (161) SSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYCQQRSSYPLTFGAGTKLELKRAA  (SEQ ID NO:9)
      human consensus(161)                   Y      V        D    K    A    L    E D               G
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